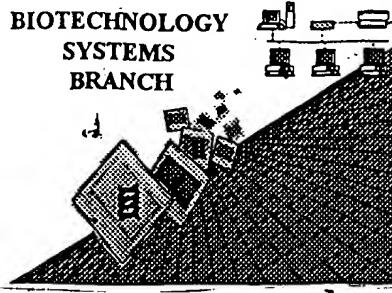


0590
1204

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/993,292
Source: O1P8
Date Processed by STIC: 12/3/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001
TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

**Does Not Comply
Corrected Diskette Needed**

Error on p. 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001
TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

57 tgtgcacgaa ccccccgttc agcccgaccg ctgcgcctta tccggtaact atcgcttga 1800
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59 cagagcgagg tatgttaggcg gtgctacaga gttcttgaag tggggccta actacggcta 1920
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104 gtcgcctccc ggagttgtc tgcagactt ttgttacccg ccaaacaaaa cccaaaaaca 4620
105 acccataccca acccaataa aacaccaaaa caagacaaat aatcattgtat tgcgtttga 4680

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

106 aatgggtaa acttgacaaa caaacccact taaaacccaa aacataccca aacacacacc 4740
 107 aaaaaaacac cataaggagt tttataatg ttggatttca ttgatgacgg ttcaacaaac 4800
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 109 ttcaacgcg agtgggcagt ctcttttgt gataaaaagg tctttaacta cacactgaac 4920
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 111 tggcaataca gcgcgttaa tgtcggttca gtgcattcag ccttactgac cagtggtctg 5040
 112 ccggtaagcg aagtggatat tggttgacaca cttcctctga cagagtatta cgacagaaat 5100
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 130 ctggataaaag ggaactcaat caagttattt tcttaccagt cattacataa tcgttattat 6180
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 134 <210> SEQ ID NO: 2
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 136 <212> TYPE: PRT
 137 <213> ORGANISM: Salmonella Typhi
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 141 1 5 10 15
 142 Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
 143 20 25 30
 144 Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
 145 35 40 45
 146 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
 147 50 55 60
 148 Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
 149 65 70 75 80
 150 Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
 151 85 90 95
 152 Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
 153 100 105 110
 154 Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
 155 115 120 125
 156 Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001
TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

157 130 135 140
158 Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
159 145 150 155 160
160 Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
161 165 170 175
162 Ala Tyr Ala Gly Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
163 180 185 190
164 Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
165 195 200 205
166 Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
167 210 215 220
168 Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
169 225 230 235 240
170 Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
171 245 250 255
172 Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
173 260 265 270
174 Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
175 275 280 285
176 Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
177 290 295 300
178 Ser
179 305
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184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Cloning primer
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191 ggatccaaaa taaggagggaa aaaaaaaaaatga ctgttatttt tgcagaacaa actgttagagg 60
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194 <210> SEQ ID NO: 4
195 <211> LENGTH: 101
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Cloning primer
202 <400> SEQUENCE: 4
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204 ttggattca ttacagggtgt taatcatttt ctggcagct c 101
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207 <211> LENGTH: 97
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Cloning primer
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001
TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

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221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Cloning primer
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232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Cloning primer
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248 <223> OTHER INFORMATION: Cloning primer
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251 cattaaaggt tatcgatgtat aagctgtcaa acatgagctt gcctaggta ttaccaatgc 60
252 ttaatcgtt aggcacctat ctcagcgatc tgtctatttc g          101
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 101
256 <212> TYPE: DNA
C--> 257 <213> ORGANISM: Artificial sequence
W--> 259 <220> FEATURE:
W--> 259 <223> OTHER INFORMATION: ← Explanation missing - see error summary
      sheet, item
259 <400> SEQUENCE: 9
260 cgaaatagac agatcgctga gataggtgcc tcactgatta agcattggta atgacctagg 60
261 cttagctcatg tttgacagct tatcatcgat aacctttaat g          101
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264 <211> LENGTH: 71
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
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269 <223> OTHER INFORMATION: Cloning primer
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273 tacacgcccattt g          71
275 <210> SEQ ID NO: 11
276 <211> LENGTH: 103
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001
TIME: 12:19:48

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:257 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:259 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:259 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:525 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...
(2253)

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/993,292

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 9 Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.